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Minimum
Maximum
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Perfect score:
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   DB DB
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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length: 2000000000
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Gapop 10.0 ,
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 2001, 15:52:41; Search time 170.72 Seconds
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G-box-binding fact
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Mopa box protein -
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alpha-globulin typ
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                                                                                                                                                                                                                                                     dog
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A;Cross-references: EMBL:X62626
C;Genetics:
A;Introns: 211/1; 269/3; 296/3; 391/3; 502/1
A;Superfamily: glycinin
C;Keywords: seed; storage protein
F;1-24/Domain: signal sequence #status predicted .
F;25-566/Product: vicilin #status predicted .MAT>

<SIG>

RESULT 1 \$22477 vicilin precursor - cacao C;Species: Theobroma cacao (cacao) C;Species: Theobroma cacao (cacao) C;Species: Theobroma cacao (cacao) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 C;Accession: \$22477; \$22478; \$18105; \$22050 R;McHenry, L.; Fritz, P.J. Plant Mol. Biol. 18, 1173-1176, 1992 Plant Mol. Biol. 18, 1173-1176, 1992 A;Title: Comparison of the structure and nucleotide A;Reference number: \$22477; MUID:92288309 A;Accession: \$22477 A;Molecule type: DNA A;Residues: 1-566 <mch> A;Cross-references: EMBL:X62625 A;Accession: \$22478 A;Molecule type: mRNA A;Residues: 1-452 <mc2> A;Cross-references: EMBL:X62626 A;Cross-references: EMBL:X62626</mc2></mch>	Þ	30 84.5 24.7 648 1 JQ1150 31 84 24.6 1761 2 T13675 32 83.5 24.4 544 1 136911 33 83.5 24.4 905 2 T23229 34 83.5 24.4 919 2 A39248 35 83 24.3 1190 2 A319205 36 83 24.3 1180 2 S69205 37 82.5 24.1 467 1 A49377 38 82.5 24.1 467 1 A49377 38 82.5 24.1 1905 2 T18267 39 82.5 24.1 1905 2 T18267 40 81.5 23.8 4957 2 T03455 41 81.5 23.8 4957 2 T03455 41 81.5 23.8 339 1 TWHU2D 42 81 23.7 339 1 TWHU2D 43 81 23.7 582 2 B53234 44 81 23.7 582 2 S05548
S22050 and nucleotide sequence of vicilin genes of coco	ALIGNMENTS	50 protein kinase (EC 175 protein L dou hypothetical protein tandrogen receptor stripe a/b protein stripe a/b protein involucrin mouse trfA protein - sli multidrug resistan ALR protein - huma ALR protein - huma transcription init vicilin-like stora hypothetical prote gap protein hunchb

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RESULT 2
$708059
alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N;Alternate names: seed storage protein
C;Species: Gossypium hirsutum (upland cotton)
C;Jate: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C;Accession: $08059
R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and germinal A; Reference number: $06398
A;Accession: $08059
A; Molecule type: DNA
A; Residues: 1-509 <CHL>
C; Superfamily: glycinin
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                                                                 A; Status: not compared with conceptual translation
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Best Local Similarity
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Pred. No. 1.3e-25;
; Mismatches 0;
                                                                                                                                 cottonseed embryogenesis and germination. XIX.
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C;Keywords: 91ycoprotein; seed; storage protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-588/Product: alpha-globulin storage proprotein #status predicted
F;417/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Mol. Biol. 7, 475-489, 1986
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII cf
A;Reference number: A30838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha-globulin B precursor (clone C72) - upland cotton
N;Alternate names: seed storage protein; vicilin precursor
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 30-Sep-1991 *sequence_revision 30-Sep-1991 *text_change 16-Jul-1999
C;Accession: A30838; 506911
R;Chlan, C. A.: Pyle, J.B.; Legocki, A.B.; Dure III, L
Plant Mol. Biol. 7, 475-489, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-605 <CHL>
A;Residues: 1-605 <CHL>
C:Superfamily: glycinin
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-605/Product: alpha-globulin type A #status predicted <MAT>
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C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C;Accession: S06398
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                                                                                                              C; Superfamily: glycinin
                                                                                                                                   C; Comment: This is a seed storage protein
                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-81 <CH2>
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A; Accession: S06911
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A;Experimental source: var. Coker 201
R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-588 < CHL>
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A; Accession: S06398
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Best Local Similarity 43.3
Conservative
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Pred. No. 1.2e-05;
14; Mismatches 18
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Pred. No. 1e-05;
12; Mismatches
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A;Genome: proc
A;Genome: proc
Mobile element: p
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A:Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera related to the Dd A:Reference number: Z14684; MUID:9819836
A:Accession: T02634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
T02634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein PV100 [imported] - winter squash
C:Species: Cucurbita maxima (winter squash)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
    밁
                                                                                                                                                                                                                                           A;Gene: rep
                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AF000580; NID:g3068582; PIDN:AAC14390.1; PID:g3068583 A;Experimental source: strain WS2162
                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-1038 < RIE>
                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: T02634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rep protein homolog - slime mold (Dictyostellum discoideum) plasmid C;Species: Dictyostellum discoideum C;Species: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-C
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A; Residues: 1-810 < YAM>
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A;Title: Multiple functional proteins are produced A;Reference number: Z22767; MUID:99107919
A;Accession: T44430
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                                                                                                         Query Match
Best Local Similarity
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Best Local Similarity 31.6
Matches 18; Conservative
                                                                                         Matches
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940 QEQQEQRERREQQEQQEQQEQQE-QQEQQEQQEQQEQQEQQEQQEQREQEEQEEQR 997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 EYEVCRLRCQVAERGVEQQRKCEQVCEERLREREQGRGEDVDEVERRDPEWEREEQR 133
                                   2 QRQYQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQERGEHENYHNHKKNRSEEEEGQQR 60
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                                                                                   Score 103.5; DB Pred. No. 0.012; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 104; DB 2; Pred. No. 0.0088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 132; DB 1; Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.; Nishimura, M.; Hara-Nishimura, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                               Length 1038;
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RESULT 8
A53185
A53185
C:pac-binding factor - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Species: Dictyostelium discoideum
C:Species: O6-Jan-1995 #sequence_revision O6-Jan-1995 #text_change 24-Sep-1999
C:Accession: A53185
R:Schnitzler, G.R.; Fischer, W.H.; Firtel, R.A.
Genes Dev. 8, 502-514, 1994
A:Fittle: Cloning and characterization of the G-box binding factor, an essenti A;Reference number: A53185; MOID:94170994
A;Reference number: A53185; MOID:94170994
A;Accession: A53185
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-708 <SCH>
A;Cross-references: GB:L29075; NID:9456561; PIDN:AAA21021.1; PID:9456562
C;Superfamily: G-box binding factor
C;Keywords: DNA binding; transcription factor; zinc finger
                                                                                                                                                                                          hypothetical protein L23H3.30 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #C:Accession: T08588 R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein 1 - African malaria mosquito (fragment)
C;Speciles: Anopholes gambiae (African malaria mosquito)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
C;Accession: S27770
R;Besansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins, F.H.
submitted to the EMBL Data Library, June 1992
A;Bescription: Distinct families of site-specific retroposons occupy identical positions A;Reference number: S27770
A;Accession: S27770
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A; Residues: 1-613 <BES>
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Best Local Similarity 31.3
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Best Local
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Pred. No. 0.08
14; Mismatches
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Pred. No. 0.017;
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0.087;
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           involucrin -
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RESULT
T14577
                                                                                                                                                                                                     A;Gene: yakA
C;Keywords: ATP; phosphoprotein; phosphotransferase;
                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1457 <KUS>
                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: T14577
                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, January 1998 A; Description: YakA, a protein kinase required for A; Reference number: Z18146
                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                    protein kinase YakA (EC 2.7.1.-) - slime mold (Dictyostelium discoideum)
C; Species: Dictyostelium discoideum
C; Species: Dictyostelium discoideum
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: DNA sequences homologous to the Drosophila A;Reference number: A26892; MUID:87257908 A;Accession: A26892
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                     R; Kuspa, A.; Lu, S.; Souza, G.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: A26892
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A; Residues: 1-139 < DUB>
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                                                                                                                    Query Match
Best Local Similarity
Matches 17; Conser
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Best Local
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ecies: Mus musculus (house mouse)
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les 18; Conser
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                                                                                  5 YQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQERGEHENYHNHKKNRSEEEEGQQR 60
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27.9%;
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Pred. No.
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Pred. No.
                                                                                                                                       Score 91;
Pred. No.
                                                   Mismatches
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                                                                                                                                                       DB 2;
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dog

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Gubbay, J.; Collignon, J.; Koopman, P.; Capel, B.; Economou, A.; Muensterberg, Nature 346, 245-250, 1990
A;Title: A gene mapping to the sex-determining region of the mouse Y chromosome A;Reference number: S10938; MUID:90326154
A;Accession: S10938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M34442; NID:g163980; PIDN:AAA30853.1; PID:g163981 C;Comment: During the terminal differentiation of keratinocytes, this protein linked envelope under the plasma membrane.
C;Superfamily: involucrin
C;Keywords: cornified cell envelope; duplication; epidermis; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOI. Biol. Evol. 7, 293-302, 1990
A:Title: The involucrin genes of pig and dog: comparison of their segments of A:Reference number: 146207; MUID:90348475
A:Accession: 146207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: I46207
R;Tseng, H.; Green, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Canis lupus familiaris (dog)
C:Date: 16-Aug-1996 #sequence_revision 23-Aug-1996 #text_change 22-Jun-1999
C:Accession: I46207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:X55491; NID:g287804; PIDN:CAA39111.1; PID:g287805
A;Note: the sequence is revised in GenBank entry MMSRVA, release 113.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-125 <GUB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:X55491; NID:g287804
A;Accession: A59162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 'TGDNCLES', 1-91 <MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Rapid evolution of the sex determining A; Reference number: S35565; MUID:93361118 A; Accession: S35565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Tucker, P.K.; Lundrigan, B.L. Nature 364, 715-717, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex-determining protein SRY - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Jan-2000
C;Accession: S35565; S10938; A59162
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A; Residues: 1-285 <TSE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: SRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: liver
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A; Residues: 1-395 < TUC>
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                                                                                      160 QQQQQFYDHHQQQQQQQQQQQQFHDHHQQKQQFHDHHQQQQQFHDHHHHHQEQQFHDHHQ 219
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                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity hes 19; Conserv
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                               QQR 60
                                                                                                                                           RQYQQCQGRCQEQQQGQREQQQC-----QRKCWEQYKEQERGEHENYHNHKKNRSEEEEG 57
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                                                                                                                                                                                               h 26.5%;
Similarity 28.6%;
18; Conservative :
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31.7%;
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                                                                                                                                                                                                    20;
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                                                                                                                                                                                               Score 90.5; DB 2;
Pred. No. 0.091;
0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               locus in Old World
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                   Length 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mice and
                                                                                                                                                                                               Gaps
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A;Title: The squence of a 32420 bp segment A; Reference number: S44537; MUID:94378722
A; Accession: S44551
                                                                                                                                     A;Cross-references: EMBL:X76053; NID:g600025; PIDN:CAA53652.1; PID:g429134 R;Brandt, T.; Christiansen, C.; Holmstroem, K.; Kallesoe, T. submitted to the Protein Sequence Database, August 1994 A;Reference number: S46157 A;Accession: S46171
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R;Coward, P; Nagai, K.; Chen, D.; Thomas, H.D.; Nagamine, C.M.; Lau, Y.F.C.
submitted to the EMBL Data Library, November 1993
A;Description: Polymorphism of a CAG trinucleotide repeat within Sry correla
A;Reference number: S78062
A;Accession: S78062
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R;Coward, P.; Nagqi, K.; Chen, D.; Thomas, H.D.; Nagamine, C.M.; Lau, Y.F.C.
Nature Genet. 6, 245-250, 1994
A;Title: Polymorphism of a CAG trinucleotide repeat within Sry correlates with B6.Y(D A;Reference number: S43344; MUID:94282071
A;Cross-references: EMBL:236158; NID:g536741; PIDN:CAA85254.1; PID:g536742; GSPDB:GN0 R;Laurent, B.C.; Treitel, M.A.; Carlson, M. Mol. Cell. Biol. 10, 5616-5625, 1990
                                                                                 A; Molecule type: DNA
A; Residues: 1-905 < BRA>
                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-905 <HOL>
                                                                                                                                                                                                                                                                                                                                       A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 30-Sep-1991 #sequence_revision 09-Sep-1994 #text_change 21-Jul-2000 C;Accession: S44551; S46171; A36375; S12067; S39145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulatory protein SNF5 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YBR2036; protein YBR289w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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C;Keywords: DNA binding
F;2-77/Domain: HMG box homology <HMGl>
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A;Residues: 1-62,'T',64-132,'L',134-142,'P',146-168,171-208,'Q',210,'Q',212-234
A;Cross-references: EMBL:U03645; NID:g460122; PIDN:AAB60446.1; PID:g460123
A;Experimental source: liver; strain Torino
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A; Residues: 1-395 < COW>
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C;Species: Mus musculus domesticus (western European house mouse)
C;Date: 25-Dec-1994 #sequence_revision 03-Nov-1995 #text_change 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: Sry
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Best Local :
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18; Conser
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A:FitLe: The SWF5 protein of Saccharomyces cerevisiae is a glutamine- and proline-rich A:Reference number: A36375; MUID:91042489
A:Accession: A36375
A:Bostdues: 1-553, 'D'.565-905 < (AUD)
A:Cennetics: A56375
A:Cennetics: A56375
A:Cennetics: A56375
A:Cennetics: A56375
A:Cennetics: A56375
A:Cennetics: A56376
A:Cennetics: A56476
A:Cennetics: A5647
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